Amendments to the Specification

Please replace paragraph [0032] with the following amended paragraph as shown:

[0032] In order to test the efficacy of the model described herein, networks with large numbers of known protein-protein interactions were utilized. For this work, ~~Saccharomyces cerviseae~~*Saccharomyces cerevisiae* protein-protein interactions taken from the Database of Interacting Proteins (DIP; ~~http://dip.doe-mbi.ucla.edu/~~) http webpage at dip doe mbi ucla edu) (Xenarios et al., 2000 Nucleic Acids Research 28:289-291) were used. The domains involved in each interaction were determined by analyzing protein sequences with hmmpfam (Bateman et al., 2000 Nucleic Acids Research 28:263-6), a publicly available software tool that referenced 2015 domains at the time of this analysis. A total of 638 protein-protein interactions (all with at least 1 domain) were analyzed, and then used to determine the domain-domain interaction probabilities. Data (in this case a list of undirected protein-protein interactions) used for studying the effect of vertex removal on network edge distributions were taken from the Fields Lab Home Page (~~http://depts.washington.edu/sfields/~~)http webpage at depts washington edu/fields.

Please replace paragraph [0044] with the following amended paragraph as shown:

[0044] A combined dataset of protein-protein interaction data for both ~~*Saccharomyces cerviseae*~~*Saccharomyces cerevisiae* and *Homo sapiens* was used. The Pfam database (Pfam 6.2; 2773 domains) and the HMMER package were used to determine the domains within each proteins (0.01 significance threshold). For the yeast data, a comprehensive list of interactions downloaded from Stanley Field's lab home page ~~(http://depts.washington.edu/sfields/)~~ (http webpage at depts washington edu/sfields) was utilized. This data included interactions from a number of sources (Xenarios et al., 2001 Nucleic Acids Research 28:289-91; Ito et al., 2000 Proc. Natl. Acad Sci. USA 97:1143-7; Uetz et al., 2000 Nature 403:623-7). A total of 708 protein-protein interactions were analyzed from yeast, all of which had at least 1 domain. For human data, a set of 778 interactions downloaded from the Myriad Genetics Pronet Online web site ~~(http://www.myriad-pronet.com/)~~ (http webpage at www myriad-pronet com/) was used. For the

analysis, an attempt was made to predict interactions in a set of 40 human proteins known to form a connected network, and which had not been included in the original training data set.

Please replace paragraph [0056] with the following amended paragraph as shown:

[0056] In this example, three different levels of protein structure in computation of P(local) are considered. The highest level corresponds to Pfam domains. These domains are specific, relatively long in length, and thus occur quite rarely within a given population of proteins. Using *Saccharomyces cerevisiae* (baker's yeast) proteome as a test system, an attempt was made to characterize a protein with at least one Pfam domain using the HIMMER-2 package (Eddy, 1998 Bioinformatics 14:755-63) at 0.001 e-value cutoff level. For the dataset containing 1771 proteins known to have at least one interaction (Stanley Field's lab homepage; ~~http://depts.washington.edu/sfields~~ http webpage at depts washington edu/sfields), it was possible to provide Pfam domains for approximately 30 percent of all yeast proteins.